

What is claimed is:

1. An isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 1;

(b) a polynucleotide comprising the nucleotide sequences of SEQ ID NO: 1 from nucleotide 161 to nucleotide 187 and nucleotide 293 to nucleotide 586;

(c) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO: 2;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 3;

(e) a polynucleotide comprising the nucleotide sequences of SEQ ID NO: 3 from nucleotide 691 to nucleotide 717 and nucleotide 823 to nucleotide 1137;

(f) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO: 4;

(g) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 5;

(h) a polynucleotide comprising the nucleotide sequences of SEQ ID NO: 5 from nucleotide 480 to nucleotide 506 and nucleotide 612 to nucleotide 923;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO: 4; and

(j) a polynucleotide that hybridizes to any one of the polynucleotides specified in (a)-(i) wherein said hybridization comprises two wash steps of 6x SSC and 65° C for 10-30 minutes.

2. The isolated polynucleotide of Claim 1 wherein the polynucleotide is operably linked to at least one regulatory element being effective in controlling expression of said isolated polynucleotide when said isolated polynucleotide is transformed into a plant.

3. An expression vector comprising the isolated polynucleotide according to Claim 1.

4. A cultured host cell transformed with the isolated polynucleotide according to Claim 2.

5. A transgenic plant comprising the isolated polynucleotide according to Claim 1.

6. A transgenic plant comprising a recombinant polynucleotide encoding a polypeptide having an AT-hook domain, wherein:

the polypeptide is overexpressed relative to a wild-type plant;

the AT-hook domain is sufficiently homologous to the AT-hook domain of SEQ ID NO: 2 that the

polypeptide binds to the narrow minor groove of AT-rich regions of DNA and regulates transcription;
 said polypeptide has the property of SEQ ID NO:2 of regulating abiotic stress tolerance or
 increasing biomass in a plant; and

wherein said binding to said DNA confers an altered trait of increased biomass or increased
 abiotic stress tolerance in said transgenic plant, as compared to a non-transformed plant that does not
 overexpress the polypeptide.

7. The transgenic plant of Claim 6, wherein said polypeptide comprises an AT-hook domain that
 is at least 78% identical to the AT-hook domain of SEQ ID NO: 2, and a second conserved domain at least
 62% identical to the second conserved domain of SEQ ID NO: 2.

8. The transgenic plant of Claim 6, wherein said recombinant polynucleotide sequence comprises
 a nucleotide sequence that hybridizes over its full length to the complement of SEQ ID NO:1, SEQ ID
 NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15
 or SEQ ID NO: 17 under stringent comprising two wash steps of 6x SSC and 65° C for 10-30 minutes.

9. The transgenic plant of Claim 6, wherein said polypeptide is selected from the group consisting
 of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ
 ID NO: 14, SEQ ID NO: 16 and SEQ ID NO: 18.

10. The transgenic plant of Claim 6, wherein said transgenic plant is characterized by altered
 sugar sensing as compared to a non-transformed plant that does not overexpress the recombinant
 polynucleotide.

11. The transgenic plant of Claim 6, wherein the transgenic plant is selected from the group
 consisting of: soybean, rice, tomato, wheat, corn, potato, cotton, oilseed rape, sunflower, alfalfa, clover,
 sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower,
 coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers,
 pineapple, pumpkin, spinach, squash, sweet corn, tobacco, watermelon, mint and other labiates, rosaceous
 fruits, and vegetable brassicas.

12. The transgenic plant of Claim 11, wherein said recombinant polynucleotide sequence
 comprises a nucleotide sequence that hybridizes over its full length to the complement of SEQ ID NO:1,

SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15 or SEQ ID NO: 17.

13. The transgenic plant of Claim 6, further comprising a constitutive, inducible, or tissue-specific promoter operably linked to said polynucleotide sequence.

14. A method for producing a transgenic plant having increased tolerance to abiotic stress, the method steps comprising:

(a) providing an expression vector comprising:

(i) a polynucleotide sequence comprising nucleotide sequences that hybridize over their full length to the complement of SEQ ID NO:1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15 or SEQ ID NO: 17 under stringent conditions comprising two wash steps of 6x SSC and 65° C for 10-30 minutes; and

(ii) one or more regulatory elements flanking the polynucleotide sequence, said one or more regulatory elements being effective to control expression of said polynucleotide sequence in a target plant;

(b) introducing the expression vector into a plant cell, and allowing the plant cell to overexpress a polypeptide encoded by the recombinant polynucleotide, said polypeptide having the property of regulating abiotic stress tolerance in a transformed plant as compared to a non-transformed plant that does not overexpress the polypeptide;

(c) growing the plant cell into a plant; and

(d) identifying an abiotic stress tolerant plant so produced with increased abiotic stress tolerance by comparing said abiotic stress tolerant plant with one or more non-transformed plants that do not overexpress the polypeptide.

15. The method of Claim 14, the method steps further comprising:

(e) selfing or crossing said abiotic stress tolerant plant with itself or another plant, respectively, to produce seed; and

(f) growing a progeny plant from the seed, thus producing a transgenic progeny plant having increased tolerance to abiotic stress.

16. The method of Claim 14, wherein:

said progeny plant expresses mRNA that encodes a DNA-binding protein having an AT-hook

domain that binds to a DNA molecule, regulates expression of said DNA molecule, and induces expression of a plant trait gene; and

said mRNA is expressed at a level greater than a non-transformed plant that does not overexpress said DNA-binding protein.

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17. The method of Claim 14, wherein said transgenic plant is selected from the group consisting of tomato, soybean and rice, and said polypeptide encoded by the recombinant polynucleotide is selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16 and SEQ ID NO: 18.

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18. A method for producing a transgenic plant having increased biomass, the method steps comprising:

(a) providing an expression vector comprising:

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(i) a polynucleotide sequence comprising a nucleotide sequence that hybridizes over its full length to the complement of SEQ ID NO:1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15 or SEQ ID NO: 17 under stringent conditions comprising two wash steps of 6x SSC and 65° C for 10-30 minutes; and
(ii) one or more regulatory elements flanking the polynucleotide sequence, said one or more regulatory elements being effective to control expression of said polynucleotide sequence in a target plant;

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(b) introducing the expression vector into a plant cell, and allowing the plant cell to overexpress a polypeptide encoded by the recombinant polynucleotide, said polypeptide having the property of increasing biomass in a transformed plant as compared to a non-transformed plant that does not overexpress the polypeptide;

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(c) growing the plant cell into a plant; and

(d) identifying one or more plants with increased biomass so produced by comparing said plant with increased biomass with one or more non-transformed plants that do not overexpress the polypeptide.

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19. The method of Claim 18, the method steps further comprising:

(e) selfing or crossing one of said plant with increased biomass with itself or another plant, respectively, to produce seed; and

(f) growing a progeny plant from the seed, thus producing a transgenic progeny plant having

increased tolerance to abiotic stress.

20. The method of Claim 19, wherein:

5 said progeny plant expresses mRNA that encodes a DNA-binding protein having an AT-hook domain that binds to a DNA molecule, regulates expression of said DNA molecule, and induces expression of a plant trait gene; and

said mRNA is expressed at a level greater than a non-transformed plant that does not overexpress said DNA-binding protein.

10 21. The method of Claim 18, wherein said transgenic plants are selected from the group consisting of tomato, soybean and rice, and said polypeptide is selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16 and SEQ ID NO: 18.